SEQUENCE LISTING

<110>   Bayer BioScience N.V.
        De Block, Marc

<120>   Methods and means for increasing the tolerance of plants to stress
conditions.

<130>   BCS 03 2002 WO1

<150>   EP03076044.1
<151>   2003-04-09

<150>   US 60/496,688
<151>   2003-08-21

<160>   25

<170>   PatentIn version 3.1

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gtg ctc cgc ggc ggc gcg ctc ttc tgg ccg ccg gcg gcg cag gag gcg        96
Val Leu Arg Gly Gly Ala Leu Phe Trp Pro Pro Ala Ala Gln Glu Ala
                20                  25                  30
ctc aag gcg ctg gcg ctg ggc ccc gac gtg agc cgc gtc tcc tcc ggc       144
Leu Lys Ala Leu Ala Leu Gly Pro Asp Val Ser Arg Val Ser Ser Gly
            35                  40                  45
gac gtc ctc gcc gac gcc ctc acc gac ctc cgc ctc gcg ctc aac ctc       192
Asp Val Leu Ala Asp Ala Leu Thr Asp Leu Arg Leu Ala Leu Asn Leu
        50                  55                  60
gac cca ctc ccg cgc cgc gcc gcc gag ggc ttc gcg ctc ttc ttc gac       240
Asp Pro Leu Pro Arg Arg Ala Ala Glu Gly Phe Ala Leu Phe Phe Asp
65                  70                  75                  80
gac ctc ctg tcg cgg gcg cag gcg cgg gac tgg ttc gac cac gtc gcc       288
Asp Leu Leu Ser Arg Ala Gln Ala Arg Asp Trp Phe Asp His Val Ala
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ccc tcc ctc gcc cgc ctc ctc ctc cgc ctc ccc acg ctg ctc gag ggc      336
Pro Ser Leu Ala Arg Leu Leu Leu Arg Leu Pro Thr Leu Leu Glu Gly
                    100                   105                   110
cac tac cgc gcc gcc ggc gac gag gct cgc ggg ctc cgc atc ctg agc      384
His Tyr Arg Ala Ala Gly Asp Glu Ala Arg Gly Leu Arg Ile Leu Ser
            115                   120                   125
tcg cag gat gcc ggg ctc gtg ctc ctc agc cag gag ctc gcc gcc gcg      432
Ser Gln Asp Ala Gly Leu Val Leu Leu Ser Gln Glu Leu Ala Ala Ala
        130                   135                   140
ctg ctc gcc tgc gcg ctc ttc tgc ctg ttc ccc acc gcc gat agg gcc      480
Leu Leu Ala Cys Ala Leu Phe Cys Leu Phe Pro Thr Ala Asp Arg Ala
145                   150                   155                   160
gag gcg tgc ctc ccg gcg atc aat ttc gat agc cta ttt gcg gca ctg      528
Glu Ala Cys Leu Pro Ala Ile Asn Phe Asp Ser Leu Phe Ala Ala Leu
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tgt tat aat tcg agg caa agc cag gag cag aag gtg agg tgc ctt gtt      576
Cys Tyr Asn Ser Arg Gln Ser Gln Glu Gln Lys Val Arg Cys Leu Val
            180                   185                   190
cac tat ttt gac agg gtg acc gct tct aca cct act ggt tcc gtt tcg      624
His Tyr Phe Asp Arg Val Thr Ala Ser Thr Pro Thr Gly Ser Val Ser
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ttt gag cgt aag gtt ctt cct cgc cgt cct gaa tct gat ggc att acg      672
Phe Glu Arg Lys Val Leu Pro Arg Arg Pro Glu Ser Asp Gly Ile Thr
        210                   215                   220
tac cct gac atg gat act tgg atg aaa tct ggt gtt ccc ctt tgc aca      720
Tyr Pro Asp Met Asp Thr Trp Met Lys Ser Gly Val Pro Leu Cys Thr
225                   230                   235                   240
ttc cgg gta ttt tcc tca ggc ttg ata gaa gat gag gaa caa gaa gcc      768
Phe Arg Val Phe Ser Ser Gly Leu Ile Glu Asp Glu Glu Gln Glu Ala
                245                   250                   255
ctt gaa gtt gac ttt gca aat aga tat ttg gga ggt ggc gca ctt tcc      816
Leu Glu Val Asp Phe Ala Asn Arg Tyr Leu Gly Gly Gly Ala Leu Ser
                260                   265                   270
aga ggc tgc gtg cag gaa gaa atc cgg ttc atg ata aac cca gaa ttg      864
Arg Gly Cys Val Gln Glu Glu Ile Arg Phe Met Ile Asn Pro Glu Leu
            275                   280                   285
atc gtg ggc atg ctc ttc atg gtt tca atg gaa gat aat gaa gct ata      912
Ile Val Gly Met Leu Phe Met Val Ser Met Glu Asp Asn Glu Ala Ile
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gaa att gtt ggt gca gaa agg ttc tca cag tac atg ggg tat ggt tcc      960
Glu Ile Val Gly Ala Glu Arg Phe Ser Gln Tyr Met Gly Tyr Gly Ser
305                   310                   315                   320
tca ttc cgt ttt act ggt gac tac tta gat agc aaa ccc ttt gat gcg     1008
Ser Phe Arg Phe Thr Gly Asp Tyr Leu Asp Ser Lys Pro Phe Asp Ala
                325                   330                   335
atg ggt aga cgg aaa act agg ata gtg gca att gat gct ttg gac tgt     1056
Met Gly Arg Arg Lys Thr Arg Ile Val Ala Ile Asp Ala Leu Asp Cys
            340                   345                   350
cca act agg tta cag ttt gaa tct agt ggt ctt cta agg gaa gtg aac     1104
Pro Thr Arg Leu Gln Phe Glu Ser Ser Gly Leu Leu Arg Glu Val Asn
            355                   360                   365
aag gct ttt tgt gga ttt ttg gat caa tca aat cat cag ctc tgt gca     1152
Lys Ala Phe Cys Gly Phe Leu Asp Gln Ser Asn His Gln Leu Cys Ala
        370                   375                   380
aag ctt gtc cag gat tta aat aca aag gat aac tgt cca agt gtc att     1200
Lys Leu Val Gln Asp Leu Asn Thr Lys Asp Asn Cys Pro Ser Val Ile
385                   390                   395                   400
cct gat gaa tgc ata gga gtt tca act gga aac tgg ggt tgc ggg gct     1248
Pro Asp Glu Cys Ile Gly Val Ser Thr Gly Asn Trp Gly Cys Gly Ala
                405                   410                   415
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ttt ggt gga aac cct gaa atc aag agc atg att caa tgg att gct gca    1296
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Ser Gln Ala Leu Arg Ser Phe Ile Asn Tyr Tyr Thr Phe Glu Ser Glu
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Ser Leu Lys Arg Leu Glu Glu Val Thr Gln Trp Ile Leu Arg His Arg
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tgg acg gtt ggc gag ttg tgg gac atg ctt gtg gag tat tca tcc cag    1440
Trp Thr Val Gly Glu Leu Trp Asp Met Leu Val Glu Tyr Ser Ser Gln
465               470               475               480
agg cta aga gga gac acc aat gag ggc ttt tta aca tgg cta ctt ccc    1488
Arg Leu Arg Gly Asp Thr Asn Glu Gly Phe Leu Thr Trp Leu Leu Pro
                485               490               495
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Lys Asp Ile Pro Asn Gly Asp Val Asp Tyr Met Cys Glu
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Leu Lys Ala Leu Ala Leu Gly Pro Asp Val Ser Arg Val Ser Ser Gly
        35   40   45

Asp Val Leu Ala Asp Ala Leu Thr Asp Leu Arg Leu Ala Leu Asn Leu
    50   55   60

Asp Pro Leu Pro Arg Arg Ala Ala Glu Gly Phe Ala Leu Phe Phe Asp
65   70   75   80

Asp Leu Leu Ser Arg Ala Gln Ala Arg Asp Trp Phe Asp His Val Ala
            85   90   95

Pro Ser Leu Ala Arg Leu Leu Leu Arg Leu Pro Thr Leu Leu Glu Gly
        100   105   110

His Tyr Arg Ala Ala Gly Asp Glu Ala Arg Gly Leu Arg Ile Leu Ser
        115   120   125

Ser Gln Asp Ala Gly Leu Val Leu Leu Ser Gln Glu Leu Ala Ala Ala
    130   135   140

Leu Leu Ala Cys Ala Leu Phe Cys Leu Phe Pro Thr Ala Asp Arg Ala
145   150   155   160

Glu Ala Cys Leu Pro Ala Ile Asn Phe Asp Ser Leu Phe Ala Ala Leu
                165   170   175

Cys Tyr Asn Ser Arg Gln Ser Gln Glu Gln Lys Val Arg Cys Leu Val
            180   185   190

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His Tyr Phe Asp Arg Val Thr Ala Ser Thr Pro Thr Gly Ser Val Ser
        195             200             205

Phe Glu Arg Lys Val Leu Pro Arg Arg Pro Glu Ser Asp Gly Ile Thr
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Tyr Pro Asp Met Asp Thr Trp Met Lys Ser Gly Val Pro Leu Cys Thr
225             230             235             240

Phe Arg Val Phe Ser Ser Gly Leu Ile Glu Asp Glu Glu Gln Glu Ala
            245             250             255

Leu Glu Val Asp Phe Ala Asn Arg Tyr Leu Gly Gly Gly Ala Leu Ser
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Arg Gly Cys Val Gln Glu Glu Ile Arg Phe Met Ile Asn Pro Glu Leu
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Ile Val Gly Met Leu Phe Met Val Ser Met Glu Asp Asn Glu Ala Ile
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Glu Ile Val Gly Ala Glu Arg Phe Ser Gln Tyr Met Gly Tyr Gly Ser
305             310             315             320

Ser Phe Arg Phe Thr Gly Asp Tyr Leu Asp Ser Lys Pro Phe Asp Ala
            325             330             335

Met Gly Arg Arg Lys Thr Arg Ile Val Ala Ile Asp Ala Leu Asp Cys
        340             345             350

Pro Thr Arg Leu Gln Phe Glu Ser Ser Gly Leu Leu Arg Glu Val Asn
        355             360             365

Lys Ala Phe Cys Gly Phe Leu Asp Gln Ser Asn His Gln Leu Cys Ala
    370             375             380

Lys Leu Val Gln Asp Leu Asn Thr Lys Asp Asn Cys Pro Ser Val Ile
385             390             395             400

Pro Asp Glu Cys Ile Gly Val Ser Thr Gly Asn Trp Gly Cys Gly Ala
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Ser Gln Ala Leu Arg Ser Phe Ile Asn Tyr Tyr Thr Phe Glu Ser Glu
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Ser Leu Lys Arg Leu Glu Glu Val Thr Gln Trp Ile Leu Arg His Arg
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Trp Thr Val Gly Glu Leu Trp Asp Met Leu Val Glu Tyr Ser Ser Gln
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